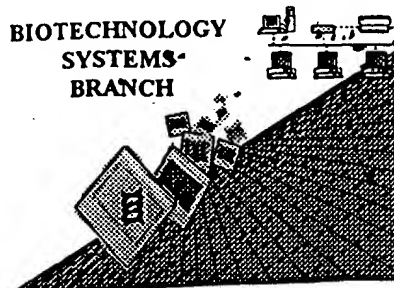


## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS-  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/918 896

Source:

OIP E

Date Processed by STIC:

02/29/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/29/2001

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PT

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length.      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped.  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
<210> sequence id number  
<400> sequence id number  
000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence.
- 11      ✓ Use of <220>      Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/918,396

DATE: 10/29/2001

TIME: 15:54:01

Input Set : A:\20162PDA - SeqList.txt

Output Set: N:\CRF3\10292001\I918396.raw

Does Not Comply  
Corrected Diskette Needed

4 <110> APPLICANT: Kennedy, Brian  
 5 Payette, Paul  
 6 Gresser, Michael  
 7 Ramachandran, Chidambaram  
 8 Tremblay, Michel  
 9 Elchebly, Mounib  
 11 <120> TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE-1B (PTP-1B)  
 12 DEFICIENT MICE AND ASSAYS FOR PTP-1B MODULATORS  
 15 <130> FILE REFERENCE: 20162PDA  
 17 <140> CURRENT APPLICATION NUMBER: 09/918,396  
 18 <141> CURRENT FILING DATE: 2001-07-30  
 20 <150> PRIOR APPLICATION NUMBER: 09/744,383  
 21 <151> PRIOR FILING DATE: 2001-01-23  
 23 <150> PRIOR APPLICATION NUMBER: 60/093,975  
 24 <151> PRIOR FILING DATE: 1998-07-24  
 26 <160> NUMBER OF SEQ ID NOS: 1  
 28 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 30 <210> SEQ ID NO: 1  
 31 <211> LENGTH: 11  
 32 <212> TYPE: PRT  
 33 <213> ORGANISM: Human  
 35 <220> FEATURE:  
 36 <223> OTHER INFORMATION: Xaa = I or V  
 38 <223> OTHER INFORMATION: Xaa = Any Amino Acid  
 40 <223> OTHER INFORMATION: Xaa = Any Amino Acid  
 42 <223> OTHER INFORMATION: Xaa = S or T  
 44 <400> SEQUENCE: 1  
 W--> 45 Xaa His Cys Xaa Ala Gly Xaa Xaa Arg Xaa Gly  
 46 1 5 10

Errored  
 Must Enumerate  
 Xaas in Fields  
 221, 222 and 223

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/918,396

DATE: 10/29/2001

TIME: 15:54:02

Input Set : A:\20162PDA - SeqList.txt

Output Set: N:\CRF3\10292001\I918396.raw

L:45 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1

L:45 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1

L:45 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1